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GAATTCGGCAGGAGCGGGTTGCAGTATGAGTCGCCAATCGGACCTAGTGAGGAGCTTCTTGAGCAGCAGGAG 75  
M S R Q S D L V R S F L E Q Q E 16

GCCCGGGACCACCGGAAGGGGGCAATCCTCGCCCGTGAGTTCAGCGACATTAAGGCCCGCTCAGTGGCTTGAAG 150  
A R D H R K G A I L A R E F S D I K A R S V A W K 41

ACTGAAGGTGTGTGCTCCACTAAAGCCGGCAGTCAGCAGGGAACTCAAAGAAGAACCCTACAAAGACGTGGTA 225  
T E G V C S T K A G S Q Q G N S K K N R Y K D V V

CCGTATGATGAGACGAGAGTCATCCTTTCCCTGCTCCAGGAGGAAGGACACGGAGATTACATTAATGCCAACTTC 300  
P Y D E T R V I L S L L Q E E G H G D Y I N A N F

ATCCGGGGCACAGATGGAAGCCAGGCCTACATTGCGACGCAAGGACCCCTGCCTCACACTCTGTTGGACTTCTGG 375  
I R G T D G S Q A Y I A T Q G P L P H T L L D F W

CGCCTGGTTTGGGAGTTTGAATCAAGGTGATCTTGATGGCCTGTGAGGAGACAGAAAATGGACGGAGGAAGTGT 450  
R L V W E F G I K V I L M A C Q E T E N G R R K C

GAACGCTACTGGGCCAGGAGCGGGAGCCTCTACAGGCCGGGCCTTTCTGCATCACCTGACAAAGGAGACAGCA 525  
E R Y W A Q E R E P L Q A G P F C I T L T K E T A

CTGACTTCGGACATCACTCTCAGGACCCCTCCAGGTTACATTCCAGAAGGAATCCCGTCCTGTGCACCAGCTACAG 600  
L T S D I T L R T L Q V T F Q K E S R P V H Q L Q

TACATGTCTTGGCCGGACCACGGGGTTCCAGCAGTTCCGATCACATTCTCACCATGGTGGAGGAGGCCCGTTGC 675  
Y M S W P D H G V P S S S D H I L T M V E E A R C

CTCCAAGGACTTGGACCTGGACCCCTCTGTGTCCACTGCAGTGCTGGCTGTGGACGAACAGGTGTCTTGTGTGCT 750  
L Q G L G P G P L C V H C S A G C G R T G V L C A

GTTGATTACGTGAGGCAGTTGCTTCTGACTCAGACAATCCCACCCAATTTCAGCCTCTTTGAAGTGGTCTGGAG 825  
V D Y V R Q L L L T Q T I P P N F S L F E V V L E

ATGCGGAAACAGCGACCTGCAGCGGTGCAGACAGAGGAGCAGTACAGGTTCTGTACCACACAGTGGCTCAGCTA 900  
M R K Q R P A A V Q T E E Q Y R F L Y H T V A Q L

TTCTCCCGCACTCTCCAGAACAACAGTCCCCTCTACCAGAACCTCAAGGAGAACCGCGCTCCAATCTGCAAGGAC 975  
F S R T L Q N N S P L Y Q N L K E N R A P I C K D

TCCTCGTCCCTCAGGACCTCCTCAGCCCTGCCTGCCACATCCCGCCCACTGGGTGGCGTTCTCAGGAGCATCTCG 1050  
S S S L R T S S A L P A T S R P L G G V L R S I S

GTGCCTGGGCCACCGACCCCTCCCATGGCTGACACTTACGCTGTGGTGCAGAAGCGTGGCGCTTCCGGCAGCACA 1125  
V P G P P T L P M A D T Y A V V Q K R G A S G S T

Fig. 1a

1007997 00502  
200709 00502

GGGCCGGGCACGCGGGCGCCCAACAGCACGGACACCCCGATCTACAGCCAGGTGGCTCCACGTATCCAGCGGCC 1200  
 G P G T R A P N S T D T P I Y S Q V A P R I Q R P  
 GTGTCACACACCGAAAACGCGCAGGGGACAACGGCACTGGGCCGAGTTCCTGCGGATGAAAACCTTCCGGGCCT 1275  
 V S H T E N A Q G T T A L G R V P A D E N P S G. P  
 GATGCCTATGAGGAAGTAACAGATGGAGCGCAGACTGGTGGGCTAGGCTTCAACTTGCGCATTGGAAGACCTAAA 1350  
 D A Y E E V T D G A Q T G G L G F N L R I G R P K  
 GGGCCACGGGATCCTCCAGCGGAGTGGACACGGGTGTAATGAGTGCTGTACCAGTTCAGCCTGTCACTCAGTGG 1425  
 G P R D P P A E W T R V  
 TGGCTGGGCGACTGCAACCCCATGCTGCTGTGTGCTGTCTTATGTATGAGTGGGACTCATGGGCCTGAATCAAA 1500  
 ATAAAAGTTTCTCAGGGTAGAAAAAACAATAGGGACTTTGGCCAGTGGTTATAGCAGTCAAAGCCAGGGGCTA 1575  
 GGAGGGGTAAAGTGGGGGAGGTGGTGGATCTACTCTGAGAAAGTTAGGAAAGCACATCAAGAGTGAGCATCGCCA 1650  
 CTCTTCTCCCCATACCTACTGGAAAGTGCACCCAGACAGAGTCCTAACTTGACAGTGCACCTCAGACAGGTC 1725  
 GCTACCTGGATGGACATGCTGGCCCTACAGCTAGAGACATGTCTAATTAGATCCTCATGTAACTTGCAATGAGC 1800  
 TAGAAAGATCTCCGTCTGGTCAGGGAAATGGATCACCTAGTCAGGTAAATAGTGTGCCATCCAGAAGACAGAACT 1875  
 GCAAGATACCGTCTTTCTCAAAATGGAAGAAAATAGATCCTCAAGAATAAATGTATGTACAATGCTCTACGCCCT 1950  
 GATCCTGCCCTGCCTCACTGCCATAATGTCACAAACAAGTCAGGGTCTATATGACAGTTGTTTCATCTAGTCAGTC 2025  
 CTGACTGTGGCCTCTGCAGGCTCAGATAGTGCCTTCTGCAGACTCTTGGAATGCCCGTCTTGAACCTTGATGAAAG 2100  
 CTTCTACCGGGAACCTGTAAACATCATTAAAATTATTAATGTAGAATTCAATAAAGAGTGGGTCAAAAACCTCAA 2175  
 AAAAAAAAAAAAAAAAAAAAAAACTCGAGAGTACTTCTAGAGCGGGCGGG 2226

Fig. 1b

<i>Fig. 2a</i>	<i>Fig. 2b</i>	<i>Fig. 2c</i>
<i>Fig. 2d</i>	<i>Fig. 2e</i>	<i>Fig. 2f</i>

*Fig. 2*

<i>Fig. 3a</i>	<i>Fig. 3b</i>
<i>Fig. 3c</i>	<i>Fig. 3d</i>

*Fig. 3*

AATTCGGGGCGCCAGTCCCGCTCCGCGCCGCGCGCTCCGCTCCGGCTCGGGCTCCGGCT  
 CGACCTCCAACCATGGCCCGTGCCAGGCGCTCGTGCTGGCACTCACCTTCCAGCTCTGC  
 1                    M A R A Q A L V L A L T F Q L C  
 GTGCCCTGCGAGTACAGCCAGGCCAGTACGATGACTTCCAGTGGGAGCAAGTGCGAATC  
 37                    V P C E Y S Q A Q Y D D Y Q W E Q V R I  
 TCCCAGCATGCCCCAGGCCAGCGAGCCCATGTCATCTTCCAGAGCCTGAGCGAGAATGAT  
 77                    S O H A P Q Q R A H V I F Q S L S E N D  
 CGCGTCTACGTGCGCGTTAATGGGGGCCCCCTGGCGAGTGCTGTGTGGAATATGACTGGA  
 117                    G V Y V R V N G G V L A S A V W N M T G  
 TATCAGGTGCTGTTTGAGGCCCTCATCTCCCCAGACCGCAGGGGCTACATGGGCCTAGAT  
 157                    Y Q V L F E A L I S P D R R G Y M G L D  
 GTGGAGGTCAACGCGGGCCAGAACGCGTCGTTCCAGTGCATGGCCGCGGGAGAGCCCATG  
 197                    V E V N A G Q N A S F Q C M A A G E P N  
 ACATCAGCCACCGGCTTCCTGGCCACTTTCCCGCTGGCTGCCGTGAGCCGCGCCGAGCAG  
 237                    T S A T G F L A T F P L A A V S R A E Q  
 ATCGTCAAGGAGCCCCAACTCCCATCGCGCCCCACAGCTGCTGCGTGCTGGCCCCACC  
 277                    I V K E P P T P I A P \_ P \_ Q \_ L \_ L \_ R \_ A \_ G \_ P \_ T \_  
 GAGATTGAGTACCGCATGGCGCGGGGCCCTGGGCTGAGGTGCACGCCGTCAGCCTGCAG  
 317                    E \_ I \_ E \_ Y \_ R \_ M \_ A \_ R \_ G \_ P \_ W \_ A \_ E \_ V \_ K \_ A \_ V \_ S \_ L \_ Q \_  
 CGTCCCGGAGACGGCGGCACTGGCCGCTGGGCCACCCCTCATCAGCCGCACCAAATGCGC  
 357                    R \_ P \_ G \_ D \_ G \_ G \_ T \_ G \_ R \_ W \_ A \_ T \_ P \_ H \_ Q \_ P \_ H \_ Q \_ M \_ R \_  
 CTGCAGTGGGAACCACTGGGCTACAACGTGACGCGTTGCCACACCTATACTGTGTGCTG  
 397                    L \_ Q \_ W \_ E \_ P \_ L \_ G \_ Y \_ N \_ V \_ T \_ R \_ C \_ H \_ T \_ Y \_ T \_ V \_ S \_ L \_  
 GAGCAAGGTGTCAGCCGCTACACCATCAAGAACCTGCTGCCCTATCGGAACGTTACGTG  
 437                    E \_ Q \_ G \_ V \_ S \_ R \_ Y \_ T \_ I \_ K \_ N \_ L \_ L \_ P \_ Y \_ R \_ N \_ V \_ H \_ V \_  
 GATGAGGATGTGCCAGTGGGATTGCAGCCGAGTCCCTGACCTTCACTCCACTGGAGGAC  
 477                    D \_ E \_ D \_ V \_ P \_ S \_ G \_ I \_ A \_ A \_ E \_ S \_ L \_ T \_ P \_ T \_ P \_ L \_ E \_ D \_

Fig. 2a

CGCCTCGGGCTGGGCTCGGGCTCCGGGGGCGGCGTCCCCGCGCCGGGCCCCGGGACGCGC 120  
 GCGCCGGAGACCGAGACTCCGGCAGCTGGCTGCACCTTCGAGGAGGCAAGTGACCCAGCA 240  
A P E T E T P A A G C T F S E A S D P A  
 CACCCTGGCACCCGGGCACCTGCGGACCTGCCCCACGGCTCCTACTTGATGGTCAACACT 361  
 H F G T R A P A D L P H G S Y L M V N T  
 ACCCACTGTGTGCAGTTTCAGCTACTTCCTGTACAGCCGGGACGGCACAGGCGGCACCCTG 481  
 T H C V Q F S Y F L Y S R D G T G G T L  
 TCCCACGGCCGTCACTGGCACCAGGCTGAGCTGGCTGTCAGCACTTTCTGGCCCAATGAA 601  
 S H G R Q W H Q A E L A V S T F W P N E  
 GACATCCTGCTTCTCAGCTACCCCTGCGCAAAGGCCCCACACTTCTCCCGCCTGGGCGAC 721  
 D I L L L S Y P C A K A P H F S R L G D  
 CGCCAACGCTTCCTCTTGCAACGGCAGAGCGGGGCCCTGGTGCCGGCCGGGGCGTTCGGC 841  
 R Q R F L L Q R Q S Q A L V P A Q A F G  
 GACCTGTACCGCTGTGTGTCCAGGCCCGCGCGGGCGGTCTCTAACTTCCCGGAGCTC 961  
 D L Y R C V S Q A P R G G V S N F A E L  
 TACCTCATCATCCAGCTCAACACCAACTCCATCATTGGCGACGGGCCGATCGTGCGCAAG 1081  
Y L I I Q L N T N S I I G D G P I V R X  
 ACCTACAAGCTGTGGCACCTCGACCCCGACACAGACTATGAGATCAGCGTGCTGCTCAGC 1201  
T Y K L W H L D P D T E Y E I S V L L T  
 AGAGCCCATGAGGGCCCCAAAGGCCTGGCTTTTGCTGAGATCCAGGCCCGTCAGCTGACC 1321  
R A H E G P K G L A F A E I Q A R Q L T  
 TGCTATCACTACACCCTGGGCAGCAGCCACAACCAGACCATCCGAGAGTGTGTGAAGACA 1441  
C Y H Y T L G S S H N Q T I R E C V K T  
 AGGCTTGTCCTCACTAACCTGAGGGGCGCAAAGAGGGCAAGGAGGTCACTTTCCAGACG 1561  
R L V L T N P E G R X E G K E V T F Q T  
 ATGATCTTCCTCAAGTGGGAGGAGCCCCAGGAGCCCAATGGTCTCATCACCCAGTATGAG 1681  
H I F L K W E E P Q E P N G L I T Q Y E

Fig. 2b

517 ATCAGCTACCAGAGCATCGAGTCATCAGACCCGGCAGTGAACGTGCCAGGCCACGACGT  
 I S Y Q S I E S S D P A V N V P G P R R  
 557 ACCTACCTGTTCTCCGTGCGGGCCCGCACAGGCAAAGGCTTCGGCCAGGCGGCACTCACT  
 T Y L F S V R A R T G K G F G Q A A L T  
 597 GCGAGTCTGAGAACACCATCACCGTGCTGCTGAGGCCGGCACAGGGCCGCGGTGCGCCC  
 G E S E N T I T V L L R P A Q G R G A P  
 637 TGGACAGGACTGCTTCCAGTGCCATTGACCTTCGAGGCGGCGCTGGCCCCAGGCTGGTG  
 W T Q L L P S A I D L R G G A G P R L V  
 677 GGTGACAACCAGACCTACCGAGGCTTCTGGAACCCACCACTTGAGCCTAGGAAGGCCAT  
 G D N Q T Y R G F W N P P L E P R K A Y  
 717 ATTGCCAGGAAAGCTGCCTGCAAGGAAAGCAAGCGGCCCTGGAGGTGTCCAGAGATCG  
 I A R K A A C K E S K R P L E V S Q R S  
 757 CTGGGTGCCATCATTGTCATCATCCGCAAAGGGAAGCCGGTGAACATGACCAAGGCCACC  
 L G A I I V I I R K G K P V N M T K A T  
 797 CAGAGCACCTGCAGGAGGACGAGCGGCTGGGCCTGTCCTTCATGGACACCCATGGCTAC  
 Q S T L Q E D E R L G L S F M D T H G Y  
 837 TCCCCGAGGCGTCCCTGTGGCCGGAAGGGCTCCCCATACCACACGGGGCAGCTGCACCCT  
 S P R R P C G R K G S P Y H T G Q L H P  
 877 GGCTTCAAGCAGGAGTATGAGAGCTTCTTTGAAGGCTGGGACGCCACAAAGAAGAAAGAC  
 G F X Q E Y E S F F E G W D A T K K K D  
 917 CACCCGATGCTGGGAGACCCCAATGCCGACTACATTAATGCCAACTACATAGATGGTTAC  
 H P M L G D P N A D Y I M A N Y I D G Y  
 957 TGGCGTATGGTGTGGCAGGAGCACTGTTCCAGCATCGTCATGATACCAAGCTGGTCGAG  
 W R M V W Q E H C S S I V M I T K L V E  
 997 AAGATTATGCTGGTGAAGACAGAGACCCTGGCTGAGTATGTCGTGCGCACTTTTGCCCTG  
 K I M L V K T E T L A E Y V V R T F A L

Fig. 2c

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ACCATCTCCAAGCTCCGCAATGAGACCTACCATGTCTTCTCCAACCTGCACCCAGGCACC 1801  
T I S K L R N E T Y H V F S N L H P G T

GAGATAACCACTAACATCTCTGCTCCCAGCTTTGATTATGCCGACATGCCGTACCCCTG 1921  
E I T T N I S A P S F D Y A D M P S P L

ATCAGTGTGTACCAGGTGATTGTGGAGGAGGAGCGGGCGCGAGGCTGCGGCGGGACGAGG 2041  
I S V Y Q V I V E E E R A R G C G G T R

CACTACTTCGGGGCCGAAGTGGCGGCCAGCAGTCTACCTGAGGCCATGCCCTTTACCGTG 2161  
H Y F G A E L A A S S L P E A M P F T V

CTCATCTACTTCCAGGCAGCAAGCCACCTGAAGGGGGAGACCCGGCTGAATTGCATCCGC 2281  
L I Y F Q A A S H L K G E T R L N C I R

GAGGAGATGGGGCTTATCCTGGGCATCTGTGCAGGGGGGCTTGCTGTCCTCATCCTTCTC 2401  
E E M G L I L G I C A G G L A V L I L L

GTCAACTACCGCCAGGAGAAGACACACATGATCAGCGCCGTGGACCGCAGCTTCACAGAC 2521  
V N Y R Q E K T H M M S A V D R S F T D

AGCACCCGGGGAGACCAGCGCAGCGGTGGGGTCACTGAGGCCAGCAGCCTCCTGGGGGGC 2541  
S T R G D Q R S G G V T E A S S L L G G

GCGGTGCGTGTGCGAGACCTTCTGCAGCACATCAACCAGATGAAGACGGCCGAGGGTTAC 2761  
A V R V A D L L Q H I N Q M K T A E G Y

AAGGTCAAGGGCAGCCGGCAGGAGCCAATGCCTGCCTATGATCGGCACCGAGTGAAACTG 2881  
K V K G S R Q E P M P A Y D R M R V X L

CACAGGTCAAACCACTTCATAGCCACTCAAGGGCCGAAGCCTGAGATGGTCTATGACTTC 3001  
H R S N H F I A T Q Q P K P E M V Y D F

GTGGGCAGGGTGAAATGCTCACGGTACTGGCCGGAGGACTCAGACACCTACGGGGACATC 3121  
V G R V K C S R Y W P E D S D T Y G D I

GAGCGGAGAGGCTACTCTGCCCGGCACGAGGTCCGCCAGTCCCACTTCACAGCGTGGCCA 3241  
E R R G Y S A R H E V R Q S H F T A W P

Fig. 2d

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1037 GAGCATGGCGTCCCCTACCATGCCACGGGGCTGCTGGCTTTCATCCGGCGGGTGAAGGCC  
E H G V P Y H A T G L L A F I R R V K A

1077 CGTTGCTATATCGTCTGGATGTGATGCTGGACATGGCAGAGTGTGAGGGCGTCTGGAC  
G C Y I V L D V M L D M A E C E G V V D

1117 CAGTACATCTTCATTCATGATGCAATCCTGGAGGCCTGCCTGTGTGGGGAGACCACCATC  
Q Y I P I H D A I L E A C L C G E T T I

1157 TCCTCCAGCTGCGGGAAGAGTTCCAGACGCTGAACTCGGTACCCCGCCGCTGGACGTG  
S S Q L R E E F Q T L N S V T P P L D V

1197 CTGCCGCCGACCGCTGCCTGCCCTTCCTCATCTCCACTGATGGGGACTCCAACAACCTAC  
L P P D R C L P F L I S T D G D S N N Y

1237 CCGCTGCAGAGCACCACGCCGACTTCTGGCGGCTGGTCTACGATTACGGGTGCACCTCC  
P L Q S T T P D F W R L V Y D Y G C T S

1277 CCAGAGCCAGGCCGGCAGCAATATGGCCTCATGGAGGTGGAGTTTATGTCGGGCACAGCT  
P E P G R Q Q Y G L M E V E F M S G T A

1317 GACCTGCTGGTGCGGCACTTCCAGTTCCTGCGCTGGTCTGCATACCGGGACACACCTGAC  
D L L V R H F Q F L R W S A Y R D T P D

1357 GATGGGCGCACCATCGTGCCTAAACGGGGGAGGACGCAGCGGCACCTTCTGCGCC  
D G R T I V H C L N G G G R S G T F C A

1397 CAAACCCTCCGGAACATAAACCACATGGTGGAGACCATGGATCAGTACCACTTTTGC  
Q T L R N Y K P N M V E T M D Q Y H F C

GGGCACCACTGCACACTCAGGGCCAGACCCACCATCCTGGACTGGCGAGGAAGATCAGT  
TCTTGCTCCCCCTTCCACTGTGGGCAGGGCCTTTCGCTTGTCCTATGGGCGGGTGGTGGG  
GTGCTGAGAGGCCTGGTGTGCTGCCTGGCAGAGTGACAAAGGCTCAGGACGGCTGGCTCTGG  
GCAGAGAGCATCCCAGGCCAAGGTTCCCACTCAGCCTGCCCCCTCTGCATGTGGGTAGAG  
AGCAGGTCTCAATTCTGATAGCCAGTGGGGCACACTGACTGTCTCTCCCAAGGGGAACCTGC  
CACTTGCTTCCCTGATATGTGCTCTGACTTCCCTGAACCAGGATCTGCCTATTACTGCTG  
CCTCTTCTTTAATCTTCAGGCCTCACTGGCCTGTCTGCTCAGCTTGGGCCAGTGACAA  
CCGTTGTGGGGAGGGGCAGTGTAGAGCAGGGCTGGTCATACCCTCTGGAGTTCAGAGCA  
TCTCTTTAAATGGGGCAGGCCACACCCCATTCGTCCTCAATTTCCCATCTGTAAA  
TGTAAGCGCTTTGTAATAAACGTGCTCTCTGAATGCCAAAAAAAAAAAAACAAAAAA

Fig. 2e



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TCCACCCACCTGATGCCGGGCCATTGTCATCCACTGCAGCGCGGGCACCGGCCGACA	3361
S T P P D A G P I V I H C S A G T G R T	
ATTTACAACCTGTGTGAAGACTCTCTGCTCCCGGCGTGTCAACATGATCCAGACTGAGGAG	3481
I Y N C V K T L C S R R V N M I Q T E E	
CCTGTCAGTGAGTTCAAGGCCACCTACAAGGAGATGATCCGCATTGATCCTCAGAGTAAT	3601
P V S E F K A T Y K E M I R I D P Q S N	
GAGGAGTGCAGCATCGCCCTGTTGCCCGGAACCGCGACAAGAACCGCAGCATGGACGTC	3721
E E C S I A L L P R N R D K N R S H D V	
ATTAATGCAGCCCTGACTGACAGCTACACACGGAGGTCGGCCTTCATGGTGACCCTGCAC	3841
I N A A L T D S Y T R R S A F M V T L H	
ATCGTCATGCTCAACCAGCTGAACCAGTCCAACCTCCGCCTGGCCCTGCCTGCAGTACTGG	3961
I V M L N Q L N Q S N S A W P C L Q Y W	
GATGAAGACTTAGTGGCTCGAGTCTTCCGGGTGCAGAACATCTCTCGGTTGCAGGAGGGA	4081
D E D L V A R V F R V Q N I S R L Q E G	
TCCAAGAAGGCCTTCTTGACCTGCTGGCTGAGGTGGACAAGTGGCAGGCCGAGAGTGGG	4201
S K K A F L H L L A E V D K W O A E S G	
TGCGCCACGGTCTGGAGATGATCCGCTGCCACAACCTGGTGGACGTTTTCTTTGCTGCC	4321
C A T V L E M I R C H N L V D V F F A A	
TACGATGTGGCCCTGGAGTACTTGGAGGGGCTGGAGTCAAGATAGCGGGGCCCTGGCCTG	4441
Y D V A L E Y L E G L E S R	
GCCTCCTGCTCTGCCCAAACACACTCCCATGGGGCAAGCACTGGAGTGGATGCTGGGCTA	4561
CCAAGGAGGAGCTTAGCAAGTCTGCACCCACCCACCTCCATAGGGTCTGCAGGCCCT	4681
GGGACTCAGGCCAAGGGGGTTGGCAGGATCCTGGGTTTTGGGAGGGATGAGTGAGGCCCT	4801
GATGTACTGGGACTTGGCATTAGGATTCCATCTGGGGGACCCCTGAAGGTCCCCCCA	4921
AGCGCCCTCCTCCCCACTGCCCCCTCCAGCCCCTGAGATATTTTGCTCACTATCCCTCCC	5041
TCCCATGGGGGGCTCCTTCCCTGCCTGACCACTGTTGCAGAAATGAAGTCACCTCGCCCC	5161
TCTGCAAGGCTGAACAACAGCCCCTGGGGTTGAGGCCCTGTGGCTCCTGGTCAGGCTGC	5281
AGAGGTAGGACCAAGTGCTTTTTTGTTCCTTTTGTATTTTGGTTGGGTGGGTGGGAAGG	5401
CTGTAGATATGACTACTGACCTACCTCGCAGGGGGCTGTGGGGAGGCATAAGCTGATGTT	5521
A	5581

Fig. 2f

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1 GAATTCGGCACGAGCGGGCTGGACCTTGCTCGCCCGCGGCCATGAGCCGCAGCCTGGACTCGG  
1 M S R S L D S

121 CGCCGGCGAGTTCAGCGACATCCAGGCCTGCTCGGCCGCCTGGAAGGCTGACGGCGTGTGCTCCA  
26 A G E F S D I Q A C S A A H K A D G V C S

241 GCCTTATGATCAGACGCGAGTAATCCTCTCCCTGCTCCAGGAAGAGGGACACAGCGACTACATTA  
66 P Y D Q T R V I L S L L Q E E G H S D Y I

361 ACCCTTGCCCTCACACCCTGCTAGACTTCTGGAGACTGGTCTGGGAGTTTGGGGTCAAGGTGATCC  
106 P L P H T L L D F W R L V W E F G V K V I

481 CCAGGAGCAGGAGCCACTGCAGACTGGGCTTTTCTGCATCACTCTGATAAAGGAGAAGTGGCTGA  
146 Q E Q E P L Q T G L F C I T L I K E K W L

601 TGTGTACCAGCTACAGTATATGTCCTGGCCAGACCGTGGGGTCCCCAGCAGTCTGACCACATGC  
186 V Y Q L Q Y M S W P D R G V P S S P D H M

721 TGTCCACTGCAGTGCGGGTTGTGGGCGAACAGGCGTCTGTGCACCGTGGATTATGTGAGGCAGC  
226 V H C S A G C G R T G V L C T V D Y V R Q

841 GATGAGGAAGCAGCGGCCTGCGGCCGTGCAGACAGAGGAGCAGTACAGGTTCTGTACCACACGG  
266 M R K Q R P A A V Q T E E Q Y R F L Y H T

961 CAAAGAGAATTGTGCCCCACTCTACGACGATGCCCTCTTCTCCGGACTCCCCAGGCACTTCTCG  
306 K E N C A P L Y D D A L F L R T P Q A L L

1081 GGGCCACGCCATGGCTGACACCTACGCGGAGGAGCAGAAGCGCGGGGCTCCAGCGGGCGCCGGGA  
346 G H A M A D T Y A E E Q K R G A P A G A G

1201 CTACAGCAAGGTGACGCCGCGCGCCAGCGACCCGGGGCGCACGCGGAGGACGCGAGGGGGACGC  
386 Y S K V T P R A Q R P G A H A E D A R G T

1321 CGTGGCGGGTGGAGCTCAGACCGTGGGCTAGGTTTCAACCTGCGCATTGGGAGGCCGAAGGGTC  
426 V A G G A Q T G G L G F N L R I G R P K G

1441 TGTTCCTCTTGTGAGCTCGGACTGCTGATGCCCCGGTGTGCTGAGCGCCGTGCCGAGAATGGA  
1561 TGCCCAATGACTGTAGCATTCAAGGCTTGAGGCTGGAGGAGGTAGCTAGGGTATAGTGGCTGGT  
1681 TTATGAAGGGGAGAAGGGACAGATGAGCTTCCGGAGACTGCTCTCCTCACCACACAGCACTAGTC  
1801 GTGGATGGACACTTCGCCATCCAGGCAGAACTAAGCCAGGCATAACCACAGCCAAGCAGATTAAC  
1921 AACCTGGACAGACAGCCAAAGCTTCAGAGATACAGTCCACAGGTGGACAAAGGATCCCCAGCCA  
2041 AAACACAGCCCCAAAGACAGACATCTCTGCTAGCTGGACAGCCAGGTGGACCCCTAAGTTAG  
2161 TCAGACCCCACTCCCTCAGGTGGGCTGGCTGGCTGACAGACCTTCTGGCCAGACAGACTCCTAAC

Fig. 3a

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CGCCGAGCTTCCTGGAGCGGCTGGAAGCGCGGGCGGCCGGGAGGGGGCAGTCCT	120
A R S F L E R L E A R G G R E G A V L	26
CCGTGGCCGGCAGTCGGCCAGAGAACGTGAGGAAGAACCGCTACAAAGACGTGCT	240
T V A G S R P E N V R K N R Y K D V L	66
ATGGCAACTTCATCCGGGGCGTGGATGGAAGCCTGGCCTACATTGCCACGCAAGG	360
N G N F I R G V D G S L A Y I A T Q G	106
TGATGGCCTGTGAGAGATAGAGAATGGGCGGAAAAGGTGTGAGCGGTACTGGGC	480
L M A C R E I E N G R K R C E R Y W A	146
ATGAGGACATCATGCTCAGGACCCTCAAGGTCACATTCCAGAAGGAGTCCCGTTC	600
N E D I M L R T L K V T F Q K E S R S	186
TCGCCATGGTGGAGGAAGCCCGTCGCCTCCAGGGATCTGGCCCTGAACCCCTCTG	720
L A M V E E A R R L Q G S G P E P L C	226
TGCTCCTGACCCAGATGATCCACCTGACTTCAGTCTCTTTGATGTGGTCCTTAA	840
L L L T Q M I P P D F S L F D V V L K	266
TGGCTCAGATGTTCTGCTCCACACTCCAGAATGCCAGCCCCACTACCAGAACAT	960
V A Q M F C S T L Q N A S P H Y Q N I	306
CCATACCCCGCCACCAGGAGGGGTCTCAGGAGCATCTCTGTGCCCGGGTCCCC	1080
A I P R P P G G V L R S I S V P G S P	346
GTGGGACGCAGACGGGGACGGGGACGGGGGCGCGCAGGGCGGAGGAGGCGCCGCT	1200
S G T Q T G T G T G A R S A E E A P L	386
TGCCTGGCCGCGTTCCTGCTGACCAAAGTCCTGCCGGATCTGGCGCTACGAGGA	1320
L P G R V P A D Q S P A G S G A Y E D	426
CCCGGGACCCGCTGCTGAGTGGACCCGGGTGTAAGTCTAACGCCAGTTCCTGCC	1440
P R D P P A E W T R V *	459
AACAGTGGGCCTGGATCAAAGTTAAAGTTTCTCAGGGTGGGAAATGTGGGGGCTT	1560
AGGCTGCACAGAGCAGATTCAAGAAAGAAGATCAGGAAGGGGCATGACCCCTGAG	1680
CATCCTCAGCACCTGAGCTCCCTCACTTGGACACTCAGGGGACCACACAGAGAA	1800
CCCAGGCAGACCGATAAAAAAGACCTCCAGATAGGCAGACAGACAGATGGACCACC	1920
GAGAGAGAGAGACCAGCCAACAGCTTGATAGACCAAGTGCAGCCAGAGAGACCACC	2040
TCAGATTACTAGACAGATATAAACAGATCCCCTGCTGAACAGATATACAGAGTTC	2160
CAACCAGATGGACTGCCAGACAGGCAGACATCAGTCCACATGGAATCCTGACATC	2280

Fig. 3b



TCCTCCAGATTGACAGACAAGTCCCCCAAATGAGTACACATCTCCAGCTATTCAG 2400  
ACTCCCAACCAGACTGACCCCTTGCTGTTACACAGCCTGCCGAGTAGCTGGGAC 2520  
ACTCCCAACCTCAAGCAATCCTCCTGCCTCAGCCTCCCAAAGTGCTGAGATTACA 2640  
CTGCTAGGATAAAACATTAAGTGGCTGTAAAAGAAATAAAAGGAGGACACGTCT 2760  
2810

*Fig. 3d*

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MCLK1	MRHSKRTYC-----PDWDERDWDYGTWRSSSSSHKRRKRSRSHSSAREOKR	43
MCLK2	P.PR.YHSSERGRSGSYHEHYQSRKHKRRR.R.WSSSSDRTRRR.REDS	50
MCLK3	H.C..YRSPEPDPLYTYRWK.RRS.SREHEGRLRYPSR.EPPPR.S---	47
MCLK4	.....H-----S.ESWGHEsy.G-----R.....TO.NRH	42
MCLK1	CRYDHSKTTDSYYLESRS INEKAYHSRRYVDEY--RNDYMGYEPGHPYGE	91
MCLK2	YHVRSSSY.DHSSDR.LY-----D.RYCGSYR....SRDRGEAY.DT	93
MCLK3	SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR-----..	94
MCLK4	..KPH.QFKDSDCHYLEARCLNERDYRD.RYIDEY-....CEGYVPRH.HR	91
MCLK1	PGSRYQMHS-SKSSGRSGRSSYKSKHRSRHHTSQHHS DGHSRHRKRSRV	140
MCLK2	DFRQSYEYHREN..Y..Q...RRKHR.R.RRSRTFSRSSSHSS.RAK-..	142
MCLK3	SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR-----..	136
MCLK4	DVESTYRIHC....V..R...P.R.RNRPCASH.S.-----I	139
MCLK1	EDDEEGHLICQSGDVLARSYEIVDTLGEAGFGKVVECIDHKVGRRVAVK	190
MCLK2	...A....YHV..W.QE.....S.....TS.R..Q...RR..T...L.	192
MCLK3	...K....V.RI.SW.QE.....GN....T.....L..ARGKSQ..L.	186
MCLK4	.....R.....GMD.LH....	189
MCLK1	IVKNVDRYCEAAQSEIQVLEHLNTTDPHSTFRCVQMLEWFEHRGHICIVF	240
MCLK2	.I...EK.K...RL..N...KI.EK..KNKNL....FD..DYH..M..S.	242
MCLK3	.IR..GH.R...RL..N..KKIKEK.KENK.L..L.SD.NFH..M..A.	236
MCLK4	....GG.R...R.....S...N.V.....D.H..V....	239
MCLK1	ELLGLSTYDFIKENSFLPFRMDHIRKMAYQICKSVNLFHSNKLTHTDLKP	290
MCLK2	.....F..L.D.NY..YPIHQV.H..F.L.QA.K...D.....	292
MCLK3	....KN.FE.L...N.Q.YPLP.V.H....L.HALR...E.Q.....	286
MCLK4	.....QI....Q.....Q.I...H.....	289
MCLK1	ENILFVKSDYTEANPKMKRDERTIVNPDIKVVDGFSATYDDEHSTLVS	340
MCLK2	.....N...ELT..LEK....SVKSTAVR.....F.H....I..	342
MCLK3	.....N..EFETL..EHKSCE.KSVK.TSIR.A.....F.H...T.I.A	336
MCLK4	.....VVK..S.....LK.T.....	339
MCLK1	TRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFPHTDSREHLAMM	390
MCLK2	.....E.....IF...V...L.Q...N.....	392
MCLK3	.....P.....E..A.....F...R...L.Q...K.....	386
MCLK4	.....Q...K.....	389
MCLK1	ERILGPLPKHMIQKTRKRRYFHHDRLDWDEHSSAGRYVSRRCPLKEFML	440
MCLK2	.....V.SR..R....QK..YRG.....NT.....REN....RRYLT	442
MCLK3	.K....I.S...HR...QK..YKGG.V...N..D....KEN....SY..	436
MCLK4	.....I.A.....K...NQ.....R.....	439
MCLK1	SQDAEHEFLFDLVGKILEYDPAKRITLKEALKHPFFFYPLKKHT	483
MCLK2	.EAED.HQ....IENM...E....L..G...Q....AC.RTEPPNTKLWD	492
MCLK4	QDSL..VQ....MRRM..F...Q...A...L....AG.TPEERSFHSSSR	486
MCLK5	CHDE...K....RRM.....R....D...Q....DL..RK	489
MCLK1	SSRDISR	499
MCLK2	NPSR	496
MCLK3		
MCLK4		

Fig. 4

SIRP4	4	MEPAGPAPGRIGPLLCQLLAASCAWSGVAGEEELQVIOPEKSVSVAAGESAHLQIVT	58
SIRP1	57	MPVPAWPHLPSPFLMTLLGLRLTGVAGEDELQVIOPEKSVSVAAGESAHLQIVT	57
		*****	
	4	SLIPVGPIQWFRGAGPARELIYNQKEGHFPRVTVTSES TKRENDFISISNITPADA	116
	1	SLIPVGPIQWFRGAGARELIYNQKEGHFPRVTVTSEL TKRNINFSISISNITPADA	115
		*****	
	4	GTYYCVKFRKGSPDT-EFKSGAGTELSVRAKPSAPVVGPAARATPOHTVSFTCESHG	173
	1	GTYYCVKFRKGSPDDVEFKSGAGTELSVRAKPSAPVVGPAVRATPEHTVSFTCESHG	173
		*****	
	4	FSPRDITLKWFKNGNELSDFQTNVDVGEESVSYSIHSTAKVVLTRQDVHSQVICEVAH	231
	1	FSPRDITLKWFKNGNELSDFQTNVDVAGCSVSYSIHSTARVVLTRQDVHSQVICEVAH	231
		*****	
	4	VTLQGDPLRG TANLSETRVPPTLEVTQQEVR AENQVNTCQVRKTFYFQRLQLTWLEN	289
	1	ITLQGDPLRG TANLSEATRVPPPTLEVTQQEVR AENQVNTCQVSNFYHRGLQLTWLEN	289
		*****	
	4	GNVSRTE TASTITENKDGTYNWM SWLLVNVSAHRDDVKLTQVEHDGQPAVSKSHDLK	347
	1	GNVSRTE TASTITENKDGTYNWM SWLLVNTCAHRDDVVLTCQVEHDGQPAVSKSYALE	347
		*****	
	4	VSAHPKEQGSNTAAENTGSNERNIYIVVGVVCTLIIVALLMAALYLVRIRQKKAQGSTS	405
	1	ISAHQKEHGS DITHPEALAPTAPLLVALLGPKLILVVGVSIAIYICWKQKA	398
		*****	
	4	STRLHEPEKNAREITQD TNDITTYADINLPKGKKPAPQAAEPNNHTEYASIQTSPPAS	463
		*****	
	4	EDTLTYADLDMVHLNRTPKQAPKPEPSFSEYASVQVPRK	503

Fig. 5